Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently Amended) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a sentinel lymph node (SLN) sample obtained from a first melanoma patient, wherein the SLN sample is histopathologically negative for melanoma cells;

(b) amplifying mRNA transcripts encoded by GalNAcT and PAX3 marker genes, the GalNAcT and PAX3 marker genes being components of a panel of marker genes from the nucleic acid from the SLN sample obtained from the first melanoma patient;

(c) detecting [[the]] levels of the mRNA transcripts encoded by the GalNAcT and PAX3 marker genes; and

(d) comparing [[levels]] the levels of the mRNA transcripts encoded by the GalNAcT and PAX3 marker genes in nucleic acid from an SLN sample obtained from a second melanoma patient to [[levels]] the levels of mRNA transcripts encoded by the GalNAcT and PAX3 marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient to predict metastatic melanoma recurrence, metastatic melanoma-free survival, overall survival, or a combination thereof, for the first melanoma patient, higher levels of the mRNA transcripts encoded by the GalNAcT and PAX3 marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient indicating that the first melanoma patient has an increased probability of metastatic melanoma recurrence as compared to the probability of metastatic melanoma recurrence of the second melanoma patient, a decreased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma patient, or a decreased probability of overall survival as compared to the probability of overall survival of the second melanoma patient, and lower levels of the mRNA transcripts encoded by the GalNAcT and PAX3 marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient indicating that the first melanoma patient has a decreased probability of metastatic melanoma recurrence as compared to the probability of metastatic

melanoma recurrence of the second melanoma patient, an increased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma patient, or an increased probability of overall survival as compared to the probability of overall survival of the second melanoma patient.

2. (Previously Presented) The method of claim 1 wherein the panel additionally comprises marker genes selected from a group consisting of MAGE-A3 and MART-1.

3. (Previously Presented) The method of claim 2 wherein the panel comprises a combination of MAGE-A3, GalNAcT, MART-1, and PAX3; or a combination of MART-1, GalNAct, and PAX3.

4. (Previously Presented) The method of claim 1 wherein the nucleic acid is mRNA and the mRNA transcripts encoded by the panel of marker genes are amplified using real-time reversal transcriptase polymerase chain reaction (qRT-PCR).

5. (Previously Presented) The method of claim 1 wherein the SLN sample is paraffin-embedded (PE) or frozen.

6. (Canceled)

7. (Previously Presented) The method of claim 1, wherein histopathology of the SLN sample is determined by hematoxylin and eosin staining or immunohistochemistry.

8.-9. (Canceled)

10. (Previously Presented) The method of claim 1, wherein the patient's prognosis is predicted for at least a three-year period following a removal of a primary tumor, sentinel lymphadenectomy (SLND), or both.

11.-34. (Canceled)

35. (Currently Amended) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a tumor-draining lymph node (TDLN) sample obtained from a first melanoma patient, wherein the TDLN sample is histopathologically negative for melanoma cells;

(b) amplifying mRNA transcripts encoded by GalNAcT and PAX3 marker genes, the GalNAcT and PAX3 marker genes being components of a panel of marker genes from the nucleic acid from the TDLN sample obtained from the first melanoma patient;

(c) detecting [[the]] levels of the mRNA transcripts encoded by the GalNAcT and PAX3; and

(d) comparing [[levels]] the levels of the mRNA transcripts encoded by the GalNAcT and PAX3 marker genes in nucleic acid from a TDLN sample obtained from a second melanoma patient to [[levels]] the levels of mRNA transcripts encoded by the GalNAcT and PAX3 marker genes in the nucleic acid from the TDLN sample obtained from the first melanoma patient to predict metastatic melanoma recurrence, metastatic melanoma-free survival, overall survival, or a combination thereof, for the first melanoma patient higher levels of the mRNA transcripts encoded by the GalNAcT and PAX3 marker genes in the nucleic acid from the TDLN sample obtained from the first melanoma patient indicating that the first melanoma patient has an increased probability of metastatic melanoma recurrent as compared to the probability of metastatic melanoma recurrence of the second melanoma patient, a decreased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma patient, or a decreased probability of overall survival as compared to the probability of overall survival of the second melanoma patient, and lower levels of the mRNA transcripts encoded by the GalNAcT and PAX3 marker genes in the nucleic acid from the TDLN sample obtained from

the first melanoma patient indicating that the first melanoma patient has a decreased probability of metastatic melanoma recurrence as compared to the probability of metastatic melanoma recurrence of the second melanoma patient, an increased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma patient, or an increased probability of overall survival as compared to the probability of overall survival of the second melanoma patient.

36. (Currently Amended) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a sentinel lymph node (SLN) sample obtained from a first melanoma patient, wherein the SLN sample is histopathologically negative for melanoma cells;

(b) amplifying mRNA transcripts encoded by GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes, the GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes being components of a panel of marker genes from the nucleic acid from the SLN sample obtained from the first melanoma patient;

(c) detecting [[the]] levels of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes; and

(d) comparing [[levels]] the levels of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes in nucleic acid from an SLN sample obtained from a second melanoma patient to [[levels]] the levels of mRNA transcripts encoded by GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient to determine whether the [[levels]] the levels of mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient are higher than the levels of mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes in the nucleic acid from the SLN sample obtained from the second melanoma patient.

37. (Previously Presented) The method of claim 36 wherein the nucleic acid is mRNA and the mRNA transcripts encoded by the marker genes are amplified using quantitative real-time reversal transcriptase polymerase chain reaction (qRT-PCR).

38. (Previously Presented) The method of claim 36 wherein the SLN sample is paraffin-embedded (PE) or frozen.

39. (Canceled)

40. (Previously Presented) The method of claim 36, wherein histopathology of the SLN sample is determined by hematoxylin and eosin staining or immunohistochemistry.

41. (Previously Presented) A method for melanoma prognosis in a patient, the method comprising:

(a) isolating nucleic acid from a sentinel lymph node (SLN) sample obtained from a melanoma patient, wherein the SLN sample is histopathologically negative for melanoma cells;

(b) amplifying mRNA transcripts encoded by a PAX3 marker gene by real-time reversal transcriptase polymerase chain reaction (qRT-PCR), the PAX3 marker gene being a component of a panel of marker genes from the nucleic acid from the SLN sample obtained from the melanoma patient; and

(c) quantifying the level of the mRNA transcripts encoded by the PAX3 marker gene by an mRNA copy number such that an mRNA copy number greater than zero indicates a poorer prognosis for the melanoma patient than a copy number of zero.

42. (Previously Presented) The method of claim 41 further comprising upstaging the prognosis for the melanoma patient if the copy number is greater than zero.

43. (Previously Presented) The method of claim 41 wherein the panel further comprises marker genes selected from a group consisting of GalNacT, MAGE-A3 and MART-1.

44. (Previously Presented) The method of claim 41 wherein the panel comprises a first combination of MAGE-A3, GalNAcT, MART-1, and PAX3; or a second combination of MART-1, GalNAct, and PAX3.

45. (Previously Presented) A method for melanoma prognosis comprising:

(a) isolating nucleic acid from a sentinel lymph node (SLN) sample obtained from a melanoma patient, wherein the SLN sample is histopathologically negative for melanoma cells;

(b) amplifying mRNA transcripts encoded by GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes by real-time reversal transcriptase polymerase chain reaction (qRT-PCR), the GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes being components of a panel of marker genes from the nucleic acid from the SLN sample obtained from the melanoma patient; and

(c) quantifying each of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes by an mRNA copy number such that a positive copy number for any of the mRNA transcripts indicates a poorer prognosis for the patient than a copy number of zero.

46. (Previously Presented) A method for melanoma prognosis comprising:

(a) isolating nucleic acid from a sentinel lymph node (SLN) sample obtained from a melanoma patient, wherein the SLN sample is histopathologically negative for melanoma cells;

(b) amplifying mRNA transcripts encoded by GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes by real-time reversal transcriptase polymerase chain reaction

(qRT-PCR), the GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes being components of a panel of marker genes from the nucleic acid from the SLN sample obtained from the melanoma patient; and

(c) quantifying each of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3 and MART-1 marker genes by an mRNA copy number, each mRNA copy number being determined from a standard curve of known copy numbers for cDNA corresponding to each gene, a positive copy number for any of the mRNA transcripts indicating a poorer prognosis for the patient than a copy number of zero.

47. (Previously Presented) The method of claim 46 further comprising upstaging the prognosis for the patient if any copy number is greater than zero.

48. (New) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a sentinel lymph node (SLN) sample obtained from a first melanoma patient, wherein the SLN sample is histopathologically negative for melanoma cells;

(b) amplifying mRNA transcripts encoded by GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes, the GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes being components of a panel of marker genes from the nucleic acid from the SLN sample obtained from the first melanoma patient;

(c) detecting levels of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes; and

(d) comparing the levels of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes in nucleic acid from an SLN sample obtained from a second melanoma patient to the levels of mRNA transcripts encoded by the GalNAcT and PAX3 marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient to predict metastatic melanoma recurrence, metastatic melanoma-free survival, overall survival, or a combination thereof, for the first melanoma patient, higher levels of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes in the nucleic acid from the SLN sample obtained from the first

melanoma patient indicating that the first melanoma patient has an increased probability of metastatic melanoma recurrence as compared to the probability of metastatic melanoma recurrence of the second melanoma patient, a decreased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma patient, or a decreased probability of overall survival as compared to the probability of overall survival of the second melanoma patient, and lower levels of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient indicating that the first melanoma patient has a decreased probability of metastatic melanoma recurrence as compared to the probability of metastatic melanoma recurrence of the second melanoma patient, an increased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma patient, or an increased probability of overall survival as compared to the probability of overall survival of the second melanoma patient.

49. (New) The method of claim 48 wherein the nucleic acid is mRNA and the mRNA transcripts encoded by the panel of marker genes are amplified using real-time reversal transcriptase polymerase chain reaction (qRT-PCR).

50. (New) The method of claim 48 wherein the SLN sample is paraffin-embedded (PE) or frozen.

51. (New) The method of claim 48 wherein histopathology of the SLN sample is determined by hematoxylin and eosin staining or immunohistochemistry.

52. (New) The method of claim 48 wherein the patient's prognosis is predicted for at least a three-year period following a removal of a primary tumor, sentinel lymphadenectomy (SLND), or both.

53. (New) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a tumor-draining lymph node (TDLN) sample obtained from a first melanoma patient, wherein the TDLN sample is histopathologically negative for melanoma cells;

(b) amplifying mRNA transcripts encoded by GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes, the GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes being components of a panel of marker genes from the nucleic acid from the TDLN sample obtained from the first melanoma patient;

(c) detecting levels of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3, and MART-1; and

(d) comparing the levels of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes in nucleic acid from a TDLN sample obtained from a second melanoma patient to the levels of mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes in the nucleic acid from the TDLN sample obtained from the first melanoma patient to predict metastatic melanoma recurrence, metastatic melanoma-free survival, overall survival, or a combination thereof, for the first melanoma patient higher levels of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes in the nucleic acid from the TDLN sample obtained from the first melanoma patient indicating that the first melanoma patient has an increased probability of metastatic melanoma recurrent as compared to the probability of metastatic melanoma recurrence of the second melanoma patient, a decreased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma patient, or a decreased probability of overall survival as compared to the probability of overall survival of the second melanoma patient, and lower levels of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes in the nucleic acid from the TDLN sample obtained from the first melanoma patient indicating that the first melanoma patient has a decreased probability of metastatic melanoma recurrence as compared to the probability of metastatic melanoma recurrence of the second melanoma patient, an increased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma

patient, or an increased probability of overall survival as compared to the probability of overall survival of the second melanoma patient.

54. (New) The method of claim 53 wherein the nucleic acid is mRNA and the mRNA transcripts encoded by the panel of marker genes are amplified using real-time reversal transcriptase polymerase chain reaction (qRT-PCR).

55. (New) The method of claim 53 wherein the SLN sample is paraffin-embedded (PE) or frozen.

56. (New) The method of claim 53 wherein histopathology of the SLN sample is determined by hematoxylin and eosin staining or immunohistochemistry.

57. (New) The method of claim 53 wherein the patient's prognosis is predicted for at least a three-year period following a removal of a primary tumor, sentinel lymphadenectomy (SLND), or both.

58. (New) A method for melanoma prognosis in a patient, the method comprising:

(a) isolating nucleic acid from a sentinel lymph node (SLN) sample obtained from a melanoma patient, wherein the SLN sample is histopathologically negative for melanoma cells;

(b) amplifying mRNA transcripts encoded by a GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes by real-time reversal transcriptase polymerase chain reaction (qRT-PCR), the GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes being a component of a panel of marker genes from the nucleic acid from the SLN sample obtained from the melanoma patient; and

(c) quantifying levels of the mRNA transcripts encoded by the GalNAcT, PAX3, MAGE-A3, and MART-1 marker genes by an mRNA copy number such that an

mRNA copy number greater than zero indicates a poorer prognosis for the melanoma patient than a copy number of zero.

59. (new) The method of claim 58 further comprising upstaging the prognosis for the melanoma patient if the copy number is greater than zero.

60. (New) The method of claim 58 wherein the nucleic acid is mRNA and the mRNA transcripts encoded by the panel of marker genes are amplified using real-time reversal transcriptase polymerase chain reaction (qRT-PCR).

61. (New) The method of claim 58 wherein the SLN sample is paraffin-embedded (PE) or frozen.

62. (New) The method of claim 58 wherein histopathology of the SLN sample is determined by hematoxylin and eosin staining or immunohistochemistry.

63. (New) The method of claim 48 wherein the patient's prognosis is predicted for at least a three-year period following a removal of a primary tumor, sentinel lymphadenectomy (SLND), or both.